

SEQUENCE LISTING

atgaaaacaat	taaaatgaca	ccagtgattc	gtggatttca	agaaaaacaa	ttgaatgtgg	1860
ttccccaaaa	agaacttgc	tgtgctgtt	tttagtcaa	cgaaaacagcg	gaaaatccat	1920
gcttagaaga	gaacgacgtt	gtgtaagtgt	tttctacgta	gattattccg	aaatatttc	1980
agtaagttct	acaccgaact	aattggtggt	tgcaagttcc	gtggaatacg	aattggtgcc	2040
aatgaaaaca	gaggagcgc	acttattatg	tacgacgcga	cgaaaaatga	atatgccgt	2100
agtttcagaa	aattgaaagt	ttttaaatat	catatttaca	gttctacaaa	aattgtacac	2160
taaataccgg	aatcgttaga	tttgaatatag	ccgcaacaga	agcgaagaat	atgttgaaac	2220
gtcttccga	taaagaacaa	aaagtcttaa	tgttcattat	cattttccaaa	cgacaaactga	2280
atgcttacgg	ttttgtgaaa	cattattgcg	atcacaccat	cggtgttagct	aatcagcata	2340
ttactttctga	aacagtccaca	aaagctttgg	catcactaag	gcacggagaa	ggatcaaac	2400
gaattttcta	tcaaatttgc	ttgaaaatca	acgcgaattt	aggaggtatt	aaccaggagc	2460
ttgactggc	agaaaattgc	gaaatattc	cagaagaaaa	agaaaagacgg	aaaacaatgc	2520
cattaactat	gtatgttgg	attgtatgtaa	ctcatccaac	ctccttcaagt	ggaattttgt	2580
attctatagc	ggctgttagt	gcgagtatca	atccagggtt	aactatctat	cggaaatatgt	2640
tttgtactca	agaagaatgt	cgtcccccgt	agcgtgcagt	ggctcatgga	cgggaaagaa	2700
cagatattt	ggaagcaaaag	ttcgtgaaat	tgctcagaga	attcgcagaa	gtgagttgtc	2760
ttgagtattt	aaaagatctc	tgggattttt	aattttttt	taaacttca	gaacaacgc	2820
aatcgagcac	cagcgcata	tgttagtctat	cgagacggag	ttagcgattc	ggagatgtca	2880
cgtgttagtc	atgatgagct	tcgatcttta	aaaagcgaag	taaaacaatt	catgtcgaa	2940
cgggatggag	aagatccaga	gccgaagtac	acgttcattt	tgatttcagaa	aagacacaat	3000
acacgattgc	ttcgaagaat	ggaaaaagat	aagccagtgg	tcaataaaga	tcttactctt	3060
gctgaaacag	atgtcgtgt	tgtctgtt	aaacaatggg	aggaggatat	gaaagaaaagc	3120
aaagaaaactg	gaattgtgaa	cccatcatcc	ggaacaactg	tggataaact	tatcgtttcg	3180
aaatacaat	tcgatttttt	cttggcatct	catcatgggt	tccttggtac	atctcgtcca	3240
ggacattaca	ctgttatgt	tgacgataaa	ggaatgagcc	aagatgaagt	ctatgtaaac	3300
gttttgaata	gcagtttagcg	attttagat	tttgtaatcc	gcatatagtt	attataaaaa	3360
aatgttttcag	aaaatgacct	acggacttgc	tttctcttct	gctagatgtc	gaaaacccat	3420
ctcggtgcct	gttcccggtt	attatgtctca	tttcatgtt	gaaaaaagcga	aagagcttta	3480
tcgaacttac	aaggAACATT	acatcggtga	ctatgcacag	ccacggactc	gacacgaaat	3540
ggAACATTT	ctccaaacta	acgtgaagta	ccctggaaat	tcgttgcatt	aacattttgc	3600
aaaagtgtcg	cccggttcaa	tcaaattttt	caattgtaga	tattgtactt	actttttttt	3660
aaagccccgt	ttcaaaaaattt	cattccatca	ctaactttt	cataaattac	ttgaaatttt	3719

<210> 2

~~<210>~~ 2
~~<211>~~ 3227

<211> 522
<213> DNA

<212> DNA
<213> *Caenorhabditis elegans*

5220>

<221> CDS

<222> (21) ... (3080)

<400> 2

```

cagccacaaa gtgatgaaac atg tcc tcg aat ttt ccc gaa ttg gaa aaa gga      53
          Met Ser Ser Asn Phe Pro Glu Leu Glu Lys Gly
          1           5           10

```

ttt tat cgt cat tct ctc gat ccg gag atg aaa tgg ctt gcg agg ccc 101
 Phe Tyr Arg His Ser Leu Asp Pro Glu Met Lys Trp Leu Ala Arg Pro
 15 20 25

act ggt aaa tgc gac ggc aaa ttc tat gag aag aaa gta ctt ctt ttg 149
 Thr Gly Lys Cys Asp Gly Lys Phe Tyr Glu Lys Lys Val Leu Leu Leu
 30 35 40

gta aat tgg ttc aag ttc tcc agc aaa att tac gat cg^g gaa tac tac 197
 Val Asn Trp Phe Lys Phe Ser Ser Lys Ile Tyr Asp Arg Glu Tyr Tyr
 45 50 55

gag tat gaa gtg aaa atg aca aag gaa gta ttg aat aga aaa cca gga 245
Glu Tyr Glu Val Lys Met Thr Lys Glu Val Leu Asn Arg Lys Pro Gly

60	65	70	75	
aaa cct ttc cca aaa aag aca gaa att cca att ccc gat cgt gca aaa Lys Pro Phe Pro Lys Lys Thr Glu Ile Pro Ile Pro Asp Arg Ala Lys 80		85	90	293
ctc ttc tgg caa cat ctt cg ^g cat gag aag aag cag aca gat ttt att Leu Phe Trp Gln His Leu Arg His Glu Lys Lys Gln Thr Asp Phe Ile 95	100		105	341
ctc gaa gac tat gtt ttt gat gaa aag gac act gtt tat agt gtt tgt Leu Glu Asp Tyr Val Phe Asp Glu Lys Asp Thr Val Tyr Ser Val Cys 110	115		120	389
cga ctg aac act gtc aca tca aaa atg ctg gtt tcg gag aaa gta gta Arg Leu Asn Thr Val Thr Ser Lys Met Leu Val Ser Glu Lys Val Val 125	130	135		437
aaa aag gat tcg gag aaa aag gat gaa aag gat ttg gag aaa aaa atc Lys Lys Asp Ser Glu Lys Lys Asp Glu Lys Asp Leu Glu Lys Lys Ile 140	145	150	155	485
tta tac aca atg ata ctt acc tat cgt aaa aaa ttt cac ctg aac ttt Leu Tyr Thr Met Ile Leu Thr Tyr Arg Lys Lys Phe His Leu Asn Phe 160		165	170	533
agt cga gaa aat ccg gaa aaa gac gaa gaa gc ^g aat cgg agt tac aaa Ser Arg Glu Asn Pro Glu Lys Asp Glu Glu Ala Asn Arg Ser Tyr Lys 175	180		185	581
ttc ctg aag aat gtt atg acc cag aaa gtt cgc tac gc ^g cct ttt gtg Phe Leu Lys Asn Val Met Thr Gln Lys Val Arg Tyr Ala Pro Phe Val 190	195		200	629
aac gag gag att aaa gta caa ttc gc ^g aaa aat ttt gtg tac gat aat Asn Glu Glu Ile Lys Val Gln Phe Ala Lys Asn Phe Val Tyr Asp Asn 205	210	215		677
aat tca att ctg cga gtt cct gaa tcg ttt cac gat cca aac aga ttc Asn Ser Ile Leu Arg Val Pro Glu Ser Phe His Asp Pro Asn Arg Phe 220	225	230	235	725
gaa caa tca tta gaa gta gca cca aga atc gaa gca tgg ttt gga att Glu Gln Ser Leu Glu Val Ala Pro Arg Ile Glu Ala Trp Phe Gly Ile 240	245		250	773
tac att gga atc aaa gaa ttg ttc gat ggt gaa cct gtg ctc aat ttt Tyr Ile Gly Ile Lys Glu Leu Phe Asp Gly Glu Pro Val Leu Asn Phe 255	260		265	821
gca att gtc gat aaa cta ttc tac aat gca ccg aaa atg tct ctt ctg Ala Ile Val Asp Lys Leu Phe Tyr Asn Ala Pro Lys Met Ser Leu Leu 270	275	280		869
gat tat ctt ctc cta att gtc gac ccc cag tcg tgt aac gat gat gta Asp Tyr Leu Leu Leu Ile Val Asp Pro Gln Ser Cys Asn Asp Asp Val 285	290	295		917
cga aaa gat ctt aaa aca aaa ctg atg gc ^g gga aaa atg aca atc aga Arg Lys Asp Leu Lys Thr Lys Leu Met Ala Gly Lys Met Thr Ile Arg 300	305	310	315	965

caa gcc gcg cg ^g cca aga att cga caa tta ttg gaa aat ttg aag ctg Gln Ala Ala Arg Pro Arg Ile Arg Gln Leu Leu Glu Asn Leu Lys Leu 320 325 330	1013
aaa tgc gca gaa gtt tgg gat aac gaa atg tcg aga ttg aca gaa cga Lys Cys Ala Glu Val Trp Asp Asn Glu Met Ser Arg Leu Thr Glu Arg 335 340 345	1061
cat ctg aca ttt cta gat ttg tgc gag gaa aac tct ctt gtt tat aaa His Leu Thr Phe Leu Asp Leu Cys Glu Glu Asn Ser Leu Val Tyr Lys 350 355 360	1109
gtc act ggt aaa tcg gac aga gga aga aat gca aaa aag tac gat act Val Thr Gly Lys Ser Asp Arg Gly Arg Asn Ala Lys Lys Tyr Asp Thr 365 370 375	1157
aca ttg ttc aaa atc tat gag gaa aac aaa aag ttc att gag ttt ccc Thr Leu Phe Lys Ile Tyr Glu Glu Asn Lys Lys Phe Ile Glu Phe Pro 380 385 390 395	1205
cac cta cca cta gtc aaa gtt aaa agt gga gca aaa gaa tac gct gta His Leu Pro Leu Val Lys Val Lys Ser Gly Ala Lys Glu Tyr Ala Val 400 405 410	1253
cca atg gaa cat ctt gaa gtt cat gag aag cca caa aga tac aag aat Pro Met Glu His Leu Glu Val His Glu Lys Pro Gln Arg Tyr Lys Asn 415 420 425	1301
cga att gat ctg gtg atg caa gac aag ttt cta aag cga gct aca cga Arg Ile Asp Leu Val Met Gln Asp Lys Phe Leu Lys Arg Ala Thr Arg 430 435 440	1349
aaa cct cac gac tac aaa gaa aat acc cta aaa atg ctg aaa gaa ttg Lys Pro His Asp Tyr Lys Glu Asn Thr Leu Lys Met Leu Lys Glu Leu 445 450 455	1397
gat ttc tct tct gaa gag cta aat ttt gtt gaa aga ttt gga tta tgc Asp Phe Ser Ser Glu Glu Leu Asn Phe Val Glu Arg Phe Gly Leu Cys 460 465 470 475	1445
tcc aaa ctt cag atg atc gaa tgt cca gga aag gtt ttg aaa gag cca Ser Lys Leu Gin Met Ile Glu Cys Pro Gly Lys Val Leu Lys Glu Pro 480 485 490	1493
atg ctt gtg aat agt gta aat gaa caa att aaa atg aca cca gtg att Met Leu Val Asn Ser Val Asn Glu Gln Ile Lys Met Thr Pro Val Ile 495 500 505	1541
cgt gga ttt caa gaa aaa caa ttg aat gtg gtt ccc gaa aaa gaa ctt Arg Gly Phe Gln Glu Lys Gln Leu Asn Val Val Pro Glu Lys Glu Leu 510 515 520	1589
tgc tgt gct gtt ttt gta gtc aac gaa aca gcg gga aat cca tgc tta Cys Cys Ala Val Phe Val Val Asn Glu Thr Ala Gly Asn Pro Cys Leu 525 530 535	1637
gaa gag aac gac gtt gtt aag ttc tac acc gaa cta att ggt ggt tgc Glu Glu Asn Asp Val Val Lys Phe Tyr Thr Glu Leu Ile Gly Gly Cys 540 545 550 555	1685

aag ttc cgt gga ata cga att ggt gcc aat gaa aac aga gga gcg caa Lys Phe Arg Gly Ile Arg Ile Gly Ala Asn Glu Asn Arg Gly Ala Gln 560 565 570	1733
tct att atg tac gac gcg acg aaa aat gaa tat gcc ttc tac aaa aat Ser Ile Met Tyr Asp Ala Thr Lys Asn Glu Tyr Ala Phe Tyr Lys Asn 575 580 585	1781
tgt aca cta aat acc gga atc ggt aga ttt gaa ata gcc gca aca gaa Cys Thr Leu Asn Thr Gly Ile Gly Arg Phe Glu Ile Ala Ala Thr Glu 590 595 600	1829
gcg aag aat atg ttt gaa cgt ctt ccc gat aaa gaa caa aaa gtc tta Ala Lys Asn Met Phe Glu Arg Leu Pro Asp Lys Glu Gln Lys Val Leu 605 610 615	1877
atg ttc att atc att tcc aaa cga caa ctg aat gct tac ggt ttt gtg Met Phe Ile Ile Ser Lys Arg Gln Leu Asn Ala Tyr Gly Phe Val 620 625 630 635	1925
aaa cat tat tgc gat cac acc atc ggt gta gct aat cag cat att act Lys His Tyr Cys Asp His Thr Ile Gly Val Ala Asn Gln His Ile Thr 640 645 650	1973
tct gaa aca gtc aca aaa gct ttg gca tca cta agg cac gag aaa gga Ser Glu Thr Val Thr Lys Ala Leu Ala Ser Leu Arg His Glu Lys Gly 655 660 665	2021
tca aaa cga att ttc tat caa att gca ttg aaa atc aac gcg aaa tta Ser Lys Arg Ile Phe Tyr Gln Ile Ala Leu Lys Ile Asn Ala Lys Leu 670 675 680	2069
gga ggt att aac cag gag ctt gac tgg tca gaa att gca gaa ata tca Gly Gly Ile Asn Gln Glu Leu Asp Trp Ser Glu Ile Ala Glu Ile Ser 685 690 695	2117
cca gaa gaa aaa gaa aga cgg aaa aca atg cca tta act atg tat gtt Pro Glu Glu Lys Glu Arg Arg Lys Thr Met Pro Leu Thr Met Tyr Val 700 705 710 715	2165
gga att gat gta act cat cca acc tcc tac agt gga att gat tat tct Gly Ile Asp Val Thr His Pro Thr Ser Tyr Ser Gly Ile Asp Tyr Ser 720 725 730	2213
ata gcg gct gta gta gcg agt atc aat cca ggt gga act atc tat cga Ile Ala Ala Val Val Ala Ser Ile Asn Pro Gly Gly Thr Ile Tyr Arg 735 740 745	2261
aat atg att gtg act caa gaa gaa tgt cgt ccc ggt gag cgt gca gtg Asn Met Ile Val Thr Gln Glu Cys Arg Pro Gly Glu Arg Ala Val 750 755 760	2309
gct cat gga cgg gaa aga aca gat att ttg gaa gca aag ttc gtg aaa Ala His Gly Arg Glu Arg Thr Asp Ile Leu Glu Ala Lys Phe Val Lys 765 770 775	2357
ttg ctc aga gaa ttc gca gaa aac aac gac aat cga gca cca gcg cat Leu Leu Arg Glu Phe Ala Glu Asn Asn Asp Asn Arg Ala Pro Ala His 780 785 790 795	2405
att gta gtc tat cga gac gga gtt agc gat tcg gag atg cta cgt gtt	2453

Ile Val Val Tyr Arg Asp Gly Val Ser Asp Ser Glu Met Leu Arg Val			
800	805	810	
agt cat gat gag ctt cga tct tta aaa agc gaa gta aaa caa ttc atg			2501
Ser His Asp Glu Leu Arg Ser Leu Lys Ser Glu Val Lys Gln Phe Met			
815	820	825	
tcg gaa cg ^g gat gga gaa gat cca gag ccg aag tac acg ttc att gtg			2549
Ser Glu Arg Asp Gly Glu Asp Pro Glu Pro Lys Tyr Thr Phe Ile Val			
830	835	840	
att cag aaa aga cac aat aca cga ttg ctt cga aga atg gaa aaa gat			2597
Ile Gln Lys Arg His Asn Thr Arg Leu Leu Arg Arg Met Glu Lys Asp			
845	850	855	
aag cca gtg gtc aat aaa gat ctt act cct gct gaa aca gat gtc gct			2645
Lys Pro Val Val Asn Lys Asp Leu Thr Pro Ala Glu Thr Asp Val Ala			
860	865	870	875
gtt gct gct gtt aaa caa tgg gag gag gat atg aaa gaa agc aaa gaa			2693
Val Ala Ala Val Lys Gln Trp Glu Glu Asp Met Lys Glu Ser Lys Glu			
880	885	890	
act gga att gtg aac cca tca tcc gga aca act gtg gat aaa ctt atc			2741
Thr Gly Ile Val Asn Pro Ser Ser Gly Thr Thr Val Asp Lys Leu Ile			
895	900	905	
gtt tcg aaa tac aaa ttc gat ttt ttc ttg gca tct cat cat ggt gtc			2789
Val Ser Lys Tyr Lys Phe Asp Phe Phe Leu Ala Ser His His Gly Val			
910	915	920	
ctt ggt aca tct cgt cca gga cat tac act gtt atg tat gac gat aaa			2837
Leu Gly Thr Ser Arg Pro Gly His Tyr Thr Val Met Tyr Asp Asp Lys			
925	930	935	
gga atg agc caa gat gaa gtc tat aaa atg acc tac gga ctt gct ttt			2885
Gly Met Ser Gln Asp Glu Val Tyr Lys Met Thr Tyr Gly Leu Ala Phe			
940	945	950	955
ctc tct gct aga tgt cga aaa ccc atc tcg ttg cct gtt ccg gtt cat			2933
Leu Ser Ala Arg Cys Arg Lys Pro Ile Ser Leu Pro Val Pro Val His			
960	965	970	
tat gct cat tta tca tgt gaa aaa gcg aaa gag ctt tat cga act tac			2981
Tyr Ala His Leu Ser Cys Glu Lys Ala Lys Glu Leu Tyr Arg Thr Tyr			
975	980	985	
aag gaa cat tac atc ggt gac tat gca cag cca cg ^g act cga cac gaa			3029
Lys Glu His Tyr Ile Gly Asp Tyr Ala Gln Pro Arg Thr Arg His Glu			
990	995	1000	
atg gaa cat ttt ctc caa act aac gtg aag tac cct gga atg tcg ttc			3077
Met Glu His Phe Leu Gln Thr Asn Val Lys Tyr Pro Gly Met Ser Phe			
1005	1010	1015	
gca taacattttg caaaaagtgtc gcccggttca atcaaatttt tcaattgttag			3130
Ala			
1020			
atatttgtact tactttttt taaagccccgg tttcaaaaaat tcattccatg actaacgttt			3190

tcataaaatta ctgtgaaattt aaaaaaaaaa aaaaaaaaa

3227

<210> 3
<211> 1020
<212> PRT
<213> Caenorhabditis elegans

<400> 3
Met Ser Ser Asn Phe Pro Glu Leu Glu Lys Gly Phe Tyr Arg His Ser
1 5 10 15
Leu Asp Pro Glu Met Lys Trp Leu Ala Arg Pro Thr Gly Lys Cys Asp
20 25 30
Gly Lys Phe Tyr Glu Lys Lys Val Leu Leu Val Asn Trp Phe Lys
35 40 45
Phe Ser Ser Lys Ile Tyr Asp Arg Glu Tyr Tyr Glu Tyr Glu Val Lys
50 55 60
Met Thr Lys Glu Val Leu Asn Arg Lys Pro Gly Lys Pro Phe Pro Lys
65 70 75 80
Lys Thr Glu Ile Pro Ile Pro Asp Arg Ala Lys Leu Phe Trp Gln His
85 90 95
Leu Arg His Glu Lys Lys Gln Thr Asp Phe Ile Leu Glu Asp Tyr Val
100 105 110
Phe Asp Glu Lys Asp Thr Val Tyr Ser Val Cys Arg Leu Asn Thr Val
115 120 125
Thr Ser Lys Met Leu Val Ser Glu Lys Val Val Lys Lys Asp Ser Glu
130 135 140
Lys Lys Asp Glu Lys Asp Leu Glu Lys Lys Ile Leu Tyr Thr Met Ile
145 150 155 160
Leu Thr Tyr Arg Lys Lys Phe His Leu Asn Phe Ser Arg Glu Asn Pro
165 170 175
Glu Lys Asp Glu Glu Ala Asn Arg Ser Tyr Lys Phe Leu Lys Asn Val
180 185 190
Met Thr Gln Lys Val Arg Tyr Ala Pro Phe Val Asn Glu Glu Ile Lys
195 200 205
Val Gln Phe Ala Lys Asn Phe Val Tyr Asp Asn Asn Ser Ile Leu Arg
210 215 220
Val Pro Glu Ser Phe His Asp Pro Asn Arg Phe Glu Gln Ser Leu Glu
225 230 235 240
Val Ala Pro Arg Ile Glu Ala Trp Phe Gly Ile Tyr Ile Gly Ile Lys
245 250 255
Glu Leu Phe Asp Gly Glu Pro Val Leu Asn Phe Ala Ile Val Asp Lys
260 265 270
Leu Phe Tyr Asn Ala Pro Lys Met Ser Leu Leu Asp Tyr Leu Leu Leu
275 280 285
Ile Val Asp Pro Gln Ser Cys Asn Asp Asp Val Arg Lys Asp Leu Lys
290 295 300
Thr Lys Leu Met Ala Gly Lys Met Thr Ile Arg Gln Ala Ala Arg Pro
305 310 315 320
Arg Ile Arg Gln Leu Leu Glu Asn Leu Lys Leu Lys Cys Ala Glu Val
325 330 335
Trp Asp Asn Glu Met Ser Arg Leu Thr Glu Arg His Leu Thr Phe Leu
340 345 350
Asp Leu Cys Glu Glu Asn Ser Leu Val Tyr Lys Val Thr Gly Lys Ser
355 360 365
Asp Arg Gly Arg Asn Ala Lys Lys Tyr Asp Thr Thr Leu Phe Lys Ile
370 375 380
Tyr Glu Glu Asn Lys Lys Phe Ile Glu Phe Pro His Leu Pro Leu Val
385 390 395 400
Lys Val Lys Ser Gly Ala Lys Glu Tyr Ala Val Pro Met Glu His Leu
405 410 415
Glu Val His Glu Lys Pro Gln Arg Tyr Lys Asn Arg Ile Asp Leu Val

420	425	430
Met Gln Asp Lys Phe Leu Lys Arg Ala Thr Arg Lys Pro His Asp Tyr		
435	440	445
Lys Glu Asn Thr Leu Lys Met Leu Lys Glu Leu Asp Phe Ser Ser Glu		
450	455	460
Glu Leu Asn Phe Val Glu Arg Phe Gly Leu Cys Ser Lys Leu Gln Met		
465	470	475
Ile Glu Cys Pro Gly Lys Val Leu Lys Glu Pro Met Leu Val Asn Ser		
485	490	495
Val Asn Glu Gln Ile Lys Met Thr Pro Val Ile Arg Gly Phe Gln Glu		
500	505	510
Lys Gln Leu Asn Val Val Pro Glu Lys Glu Leu Cys Cys Ala Val Phe		
515	520	525
Val Val Asn Glu Thr Ala Gly Asn Pro Cys Leu Glu Glu Asn Asp Val		
530	535	540
Val Lys Phe Tyr Thr Glu Leu Ile Gly Gly Cys Lys Phe Arg Gly Ile		
545	550	555
Arg Ile Gly Ala Asn Glu Asn Arg Gly Ala Gln Ser Ile Met Tyr Asp		
565	570	575
Ala Thr Lys Asn Glu Tyr Ala Phe Tyr Lys Asn Cys Thr Leu Asn Thr		
580	585	590
Gly Ile Gly Arg Phe Glu Ile Ala Ala Thr Glu Ala Lys Asn Met Phe		
595	600	605
Glu Arg Leu Pro Asp Lys Glu Gln Lys Val Leu Met Phe Ile Ile Ile		
610	615	620
Ser Lys Arg Gln Leu Asn Ala Tyr Gly Phe Val Lys His Tyr Cys Asp		
625	630	635
His Thr Ile Gly Val Ala Asn Gln His Ile Thr Ser Glu Thr Val Thr		
645	650	655
Lys Ala Leu Ala Ser Leu Arg His Glu Lys Gly Ser Lys Arg Ile Phe		
660	665	670
Tyr Gln Ile Ala Leu Lys Ile Asn Ala Lys Leu Gly Gly Ile Asn Gln		
675	680	685
Glu Leu Asp Trp Ser Glu Ile Ala Glu Ile Ser Pro Glu Glu Lys Glu		
690	695	700
Arg Arg Lys Thr Met Pro Leu Thr Met Tyr Val Gly Ile Asp Val Thr		
705	710	715
His Pro Thr Ser Tyr Ser Gly Ile Asp Tyr Ser Ile Ala Ala Val Val		
725	730	735
Ala Ser Ile Asn Pro Gly Gly Thr Ile Tyr Arg Asn Met Ile Val Thr		
740	745	750
Gln Glu Glu Cys Arg Pro Gly Glu Arg Ala Val Ala His Gly Arg Glu		
755	760	765
Arg Thr Asp Ile Leu Glu Ala Lys Phe Val Lys Leu Leu Arg Glu Phe		
770	775	780
Ala Glu Asn Asn Asp Asn Arg Ala Pro Ala His Ile Val Val Tyr Arg		
785	790	795
Asp Gly Val Ser Asp Ser Glu Met Leu Arg Val Ser His Asp Glu Leu		
805	810	815
Arg Ser Leu Lys Ser Glu Val Lys Gln Phe Met Ser Glu Arg Asp Gly		
820	825	830
Glu Asp Pro Glu Pro Lys Tyr Thr Phe Ile Val Ile Gln Lys Arg His		
835	840	845
Asn Thr Arg Leu Leu Arg Arg Met Glu Lys Asp Lys Pro Val Val Asn		
850	855	860
Lys Asp Leu Thr Pro Ala Glu Thr Asp Val Ala Val Ala Val Lys		
865	870	875
Gln Trp Glu Glu Asp Met Lys Glu Ser Lys Glu Thr Gly Ile Val Asn		
885	890	895
Pro Ser Ser Gly Thr Thr Val Asp Lys Leu Ile Val Ser Lys Tyr Lys		
900	905	910

Phe	Asp	Phe	Phe	Leu	Ala	Ser	His	His	Gly	Val	Leu	Gly	Thr	Ser	Arg
915							920					925			
Pro	Gly	His	Tyr	Thr	Val	Met	Tyr	Asp	Asp	Lys	Gly	Met	Ser	Gln	Asp
930						935					940				
Glu	Val	Tyr	Lys	Met	Thr	Tyr	Gly	Leu	Ala	Phe	Leu	Ser	Ala	Arg	Cys
945						950				955			960		
Arg	Lys	Pro	Ile	Ser	Leu	Pro	Val	Pro	Val	His	Tyr	Ala	His	Leu	Ser
						965			970			975			
Cys	Glu	Lys	Ala	Lys	Glu	Leu	Tyr	Arg	Thr	Tyr	Lys	Glu	His	Tyr	Ile
						980			985			990			
Gly	Asp	Tyr	Ala	Gln	Pro	Arg	Thr	Arg	His	Glu	Met	Glu	His	Phe	Leu
						995			1000			1005			
Gln	Thr	Asn	Val	Lys	Tyr	Pro	Gly	Met	Ser	Phe	Ala				
						1010			1015			1020			

<210> 4

<211> 1222

<212> DNA

<213> Caenorhabditis elegans

<400> 4

atggatttaa	ccaaactaac	gtttgaaagc	gttttcggtg	gatcagatgt	tccttatgaag	60
ccttcccgat	cgaggataa	caaaaacgcca	agaaaacagaa	cagatttgg	gatgtttctgt	120
aagaaaactc	ccctcatggt	actagaagag	gctgctaagg	ctgtctatca	aaagacgcca	180
acttggggca	ctgtcgaact	tcctgaaggc	ttcgagatga	cgttggattct	aatgtgaard	240
actgtaaaag	gcaggcaac	aagcaagaaa	gctgcgagac	aaaaggctgc	tgttgaatat	300
ttacgcagg	tttgtggagaa	agggaaagcac	gaaatctttt	tcatttcctgg	aacaaccaaa	360
gaagaagctc	tttgcataat	tgatcaaata	tcggataagg	ctgaggaaatt	gaaacgatca	420
acttcagat	ctgttcagg	taacgataac	gatgattcga	ttccttacaag	tgttgaattt	480
ccacctggta	tttcgccaac	cgagaatgg	gtcgaaagt	tgcaggaaaa	atctcaaaaa	540
agcaagctgc	aaggccccat	ctatgaagat	tccaagaatg	agagaaccga	gcgtttcttg	600
gttatatgca	cgatgtgca	tcaaaaacc	agagaatca	gaagtaagaa	gaaggacgca	660
aagaatcttgc	cagcatgg	gatgtggaaa	gcgttggag	acggatcgat	atctctggaa	720
tcatacatgata	tgttgcgtgt	gattgaaaat	ttgaaagaag	ctgaacattt	actcgaaatt	780
caggatcaag	catccaagat	taaagacaag	cattccgcac	tgattgatat	actctcgac	840
aagaaaagat	tttcagacta	cagcatggat	ttcaacgtat	tatcgttag	cacaatggga	900
atacatcagg	tgttatttgg	aatctcgatc	cggcgatctag	tttctccaga	ccccgacgat	960
ttggaaatgg	qagcagaaca	cacccagact	qaagaaatta	tgaaggctac	tgccgagaag	1020
gaaaagctac	ggaagaagaa	tatgccagat	tccggccgc	tagtgtttgc	tggacatgtt	1080
tcatcgccgg	aaggcgctaa	acagtgtgt	tgttaatcgg	cgattatcca	tttcaacacc	1140
tatgatttca	cggattgaaa	atattattgc	gtattcctga	aaaatgaagc	gtctgaatga	1200
ttataaaaaaa	aaaaaaaaaa	aa				1222

<210> 5

<211> 407

<212> PRT

<213> Caenorhabditis elegans

<220>

<221> VARIANT

<222> (1)...(407)

<223> Xaa = Any Amino Acid

<400> 5

Met	Asp	Leu	Thr	Lys	Leu	Thr	Phe	Glu	Ser	Val	Phe	Gly	Gly	Ser	Asp
1					5				10			15			
Val	Pro	Met	Lys	Pro	Ser	Arg	Ser	Glu	Asp	Asn	Lys	Thr	Pro	Arg	Asn
							20			25			30		
Arg	Thr	Asp	Leu	Glu	Met	Phe	Leu	Lys	Lys	Thr	Pro	Leu	Met	Val	Leu
							35		40			45			
Glu	Glu	Ala	Ala	Lys	Ala	Val	Tyr	Gln	Lys	Thr	Pro	Thr	Trp	Gly	Thr

50	55	60
Val Glu Leu Pro Glu Gly Phe Glu Met Thr Leu Ile Leu Asn Glu Ile		
65	70	75
Thr Val Lys Gly Gln Ala Thr Ser Lys Lys Ala Ala Arg Gln Lys Ala		
85	90	95
Ala Val Glu Tyr Leu Arg Lys Val Val Glu Lys Gly Lys His Glu Ile		
100	105	110
Phe Phe Ile Pro Gly Thr Thr Lys Glu Glu Ala Leu Ser Asn Ile Asp		
115	120	125
Gln Ile Ser Asp Lys Ala Glu Glu Leu Lys Arg Ser Thr Ser Asp Ala		
130	135	140
Val Gln Asp Asn Asp Asn Asp Ser Ile Pro Thr Ser Ala Glu Phe		
145	150	155
Pro Pro Gly Ile Ser Pro Thr Glu Asn Trp Val Gly Lys Leu Gln Glu		
165	170	175
Lys Ser Gln Lys Ser Lys Leu Gln Ala Pro Ile Tyr Glu Asp Ser Lys		
180	185	190
Asn Glu Arg Thr Glu Arg Phe Leu Val Ile Cys Thr Met Cys Asn Gln		
195	200	205
Lys Thr Arg Gly Ile Arg Ser Lys Lys Asp Ala Lys Asn Leu Ala		
210	215	220
Ala Trp Leu Met Trp Lys Ala Leu Glu Asp Gly Ile Glu Ser Leu Glu		
225	230	235
Ser Tyr Asp Met Val Asp Val Ile Glu Asn Leu Glu Glu Ala Glu His		
245	250	255
Leu Leu Glu Ile Gln Asp Gln Ala Ser Lys Ile Lys Asp Lys His Ser		
260	265	270
Ala Leu Ile Asp Ile Leu Ser Asp Lys Lys Arg Phe Ser Asp Tyr Ser		
275	280	285
Met Asp Phe Asn Val Leu Ser Val Ser Thr Met Gly Ile His Gln Val		
290	295	300
Leu Leu Glu Ile Ser Phe Arg Arg Leu Val Ser Pro Asp Pro Asp Asp		
305	310	315
Leu Glu Met Gly Ala Glu His Thr Gln Thr Glu Glu Ile Met Lys Ala		
325	330	335
Thr Ala Glu Lys Glu Lys Leu Arg Lys Lys Asn Met Pro Asp Ser Gly		
340	345	350
Pro Leu Val Phe Ala Gly His Gly Ser Ser Ala Glu Glu Ala Lys Gln		
355	360	365
Cys Ala Cys Lys Ser Ala Ile Ile His Phe Asn Thr Tyr Asp Phe Thr		
370	375	380
Asp Xaa Lys Tyr Tyr Cys Val Phe Leu Lys Asn Glu Ala Ser Glu Xaa		
385	390	395
Leu Xaa Lys Lys Lys Lys Lys		
405		

<210> 6

<211> 763

<212> PRT

<213> Arabidopsis thaliana

<400> 6

Gly Ile Ile Asn Gly Pro Lys Arg Glu Arg Ser Tyr Lys Val Ala Ile		
1	5	10
Lys Phe Val Ala Arg Ala Asn Met His His Leu Gly Glu Phe Leu Ala		
20	25	30
Gly Lys Arg Ala Asp Cys Pro Gln Glu Ala Val Gln Ile Leu Asp Ile		
35	40	45
Val Leu Arg Glu Leu Ser Val Lys Arg Phe Cys Pro Val Gly Arg Ser		
50	55	60
Phe Phe Ser Pro Asp Ile Lys Thr Pro Gln Arg Leu Gly Glu Gly Leu		

65	70	75	80
Glu Ser Trp Cys Gly Phe Tyr Gln Ser Ile Arg Pro Thr Gln Met Gly			
85	90	95	
Leu Ser Leu Asn Ile Asp Met Ala Ser Ala Ala Phe Ile Glu Pro Leu			
100	105	110	
Pro Val Ile Glu Phe Val Ala Gln Leu Leu Gly Lys Asp Val Leu Ser			
115	120	125	
Lys Pro Leu Ser Asp Ser Asp Arg Val Lys Ile Lys Lys Gly Leu Arg			
130	135	140	
Gly Val Lys Val Glu Val Thr His Arg Ala Asn Val Arg Arg Lys Tyr			
145	150	155	160
Arg Val Ala Gly Leu Thr Thr Gln Pro Thr Arg Glu Leu Met Phe Pro			
165	170	175	
Val Asp Glu Asn Cys Thr Met Lys Ser Val Ile Glu Tyr Phe Gln Glu			
180	185	190	
Met Tyr Gly Phe Thr Ile Gln His Thr His Leu Pro Cys Leu Gln Val			
195	200	205	
Gly Asn Gln Lys Lys Ala Ser Tyr Leu Pro Met Glu Ala Cys Lys Ile			
210	215	220	
Val Glu Gly Gln Arg Tyr Thr Lys Arg Leu Asn Glu Lys Gln Ile Thr			
225	230	235	240
Ala Leu Leu Lys Val Thr Cys Gln Arg Ala Glu Gly Gln Arg Asn Asp			
245	250	255	
Ile Leu Arg Thr Val Gln His Asn Ala Tyr Asp Gln Asp Pro Tyr Ala			
260	265	270	
Lys Glu Phe Gly Met Asn Ile Ser Glu Lys Leu Ala Ser Val Glu Ala			
275	280	285	
Arg Ile Leu Pro Ala Pro Trp Leu Lys Tyr His Glu Asn Gly Lys Glu			
290	295	300	
Lys Asp Cys Leu Pro Gln Val Gly Gln Trp Asn Met Met Asn Lys Lys			
305	310	315	320
Met Ile Asn Gly Met Thr Val Ser Arg Trp Ala Cys Val Asn Phe Ser			
325	330	335	
Arg Ser Val Gln Glu Asn Val Ala Arg Gly Phe Cys Asn Glu Leu Gly			
340	345	350	
Gln Met Cys Glu Val Ser Gly Met Glu Phe Asn Pro Glu Pro Val Ile			
355	360	365	
Pro Ile Tyr Ser Ala Arg Pro Asp Gln Val Glu Lys Ala Leu Lys His			
370	375	380	
Val Tyr His Thr Ser Met Asn Lys Thr Lys Gly Lys Glu Leu Glu Leu			
385	390	395	400
Leu Leu Ala Ile Leu Pro Asp Asn Asn Gly Ser Leu Tyr Gly Asp Leu			
405	410	415	
Lys Arg Ile Cys Glu Thr Glu Leu Gly Leu Ile Ser Gln Cys Cys Leu			
420	425	430	
Thr Lys His Val Phe Lys Ile Ser Lys Gln Tyr Leu Ala Asp Val Ser			
435	440	445	
Leu Lys Ile Asn Val Lys Met Gly Gly Arg Asn Thr Val Leu Val Asp			
450	455	460	
Ala Ile Ser Cys Arg Ile Pro Leu Val Ser Asp Ile Pro Thr Ile Ile			
465	470	475	480
Phe Gly Ala Asp Val Thr His Pro Glu Asn Gly Glu Glu Ser Ser Pro			
485	490	495	
Ser Ile Ala Ala Val Val Ala Ser Gln Asp Trp Pro Glu Val Thr Lys			
500	505	510	
Tyr Ala Gly Leu Val Cys Ala Gln Ala His Arg Gln Glu Leu Ile Gln			
515	520	525	
Asp Leu Tyr Lys Thr Trp Gln Asp Pro Val Arg Gly Thr Val Ser Gly			
530	535	540	
Gly Met Ile Arg Asp Leu Leu Ile Ser Phe Arg Lys Ala Thr Gly Gln			
545	550	555	560

```

<210> 7
<211> 678
<212> PRT
<213> Drosophila melanogaster

<400> 7
Arg Ala Gly Glu Asn Ile Glu Ile Lys Ile Lys Ala Val Gly Ser Val
      1           5           10          15
Gln Ser Thr Asp Ala Glu Gln Phe Gln Val Leu Asn Leu Ile Leu Arg
      20          25          30
Arg Ala Met Glu Gly Leu Asp Leu Lys Leu Val Ser Arg Tyr Tyr Tyr
      35          40          45
Asp Pro Gln Ala Lys Ile Asn Leu Glu Asn Phe Arg Met Gln Leu Trp
      50          55          60
Pro Gly Tyr Gln Thr Ser Ile Arg Gln His Glu Asn Asp Ile Leu Leu
      65          70          75          80
Cys Ser Glu Ile Cys His Lys Val Met Arg Thr Glu Thr Leu Tyr Asn
      85          90          95
Ile Leu Ser Asp Ala Ile Arg Asp Ser Asp Asp Tyr Gln Ser Thr Phe
      100         105         110
Lys Arg Ala Val Met Gly Met Val Ile Leu Thr Asp Tyr Asn Asn Lys
      115         120         125
Thr Tyr Arg Ile Asp Asp Val Asp Phe Gln Ser Thr Pro Leu Cys Lys
      130         135         140
Phe Lys Thr Asn Asp Gly Glu Ile Ser Tyr Val Asp Tyr Tyr Lys Lys
      145         150         155         160
Arg Tyr Asn Ile Ile Arg Asp Leu Lys Gln Pro Leu Val Met Ser
      165         170         175
Arg Pro Thr Asp Lys Asn Ile Arg Gly Gly Asn Asp Gln Ala Ile Met
      180         185         190
Ile Ile Pro Glu Leu Ala Arg Ala Thr Gly Met Thr Asp Ala Met Arg
      195         200         205
Ala Asp Phe Arg Thr Leu Arg Ala Met Ser Glu His Thr Arg Leu Asn
      210         215         220

```

Pro Asp Arg Arg Ile Glu Arg Leu Arg Met Phe Asn Lys Arg Leu Lys
 225 230 235 240
 Ser Cys Lys Gln Ser Val Glu Thr Leu Lys Ser Trp Asn Ile Glu Leu
 245 250 255
 Asp Ser Ala Leu Val Glu Ile Pro Ala Arg Val Leu Pro Pro Glu Lys
 260 265 270
 Ile Leu Phe Gly Asn Gln Lys Ile Phe Val Cys Asp Ala Arg Ala Asp
 275 280 285
 Trp Thr Asn Glu Phe Arg Thr Cys Ser Met Phe Lys Asn Val His Ile
 290 295 300
 Asn Arg Trp Tyr Val Ile Thr Pro Ser Arg Asn Leu Arg Glu Thr Gln
 305 310 315 320
 Glu Phe Val Gln Met Cys Ile Arg Thr Ala Ser Ser Met Lys Met Asn
 325 330 335
 Ile Cys Asn Pro Ile Tyr Glu Glu Ile Pro Asp Asp Arg Asn Gly Thr
 340 345 350
 Tyr Ser Gln Ala Ile Asp Asn Ala Ala Asn Asp Pro Gln Ile Val
 355 360 365
 Met Val Val Met Arg Ser Pro Asn Glu Glu Lys Tyr Ser Cys Ile Lys
 370 375 380
 Lys Arg Thr Cys Val Asp Arg Pro Val Pro Ser Gln Val Val Thr Leu
 385 390 395 400
 Lys Val Ile Ala Pro Arg Gln Gln Lys Pro Thr Gly Leu Met Ser Ile
 405 410 415
 Ala Thr Lys Val Val Ile Gln Met Asn Ala Lys Leu Met Gly Ala Pro
 420 425 430
 Trp Gln Val Val Ile Pro Leu His Gly Leu Met Thr Val Gly Phe Asp
 435 440 445
 Val Cys His Ser Pro Lys Asn Lys Asn Lys Ser Tyr Gly Ala Phe Val
 450 455 460
 Ala Thr Met Asp Gln Lys Glu Ser Phe Arg Tyr Phe Ser Thr Val Asn
 465 470 475 480
 Glu His Ile Lys Gly Gln Glu Leu Ser Glu Gln Met Ser Val Asn Met
 485 490 495
 Ala Cys Ala Leu Arg Ser Tyr Gln Glu Gln His Arg Ser Leu Pro Glu
 500 505 510
 Arg Ile Leu Phe Phe Arg Asp Gly Val Gly Asp Gly Gln Leu Tyr Gln
 515 520 525
 Val Val Asn Ser Glu Val Asn Thr Leu Lys Asp Arg Leu Asp Glu Ile
 530 535 540
 Tyr Lys Ser Ala Gly Lys Gln Glu Gly Cys Arg Met Thr Phe Ile Ile
 545 550 555 560
 Val Ser Lys Arg Ile Asn Ser Arg Tyr Phe Thr Gly His Arg Asn Pro
 565 570 575
 Val Pro Gly Thr Val Val Asp Asp Val Ile Thr Leu Pro Glu Arg Tyr
 580 585 590
 Asp Phe Phe Leu Val Ser Gln Ala Val Arg Ile Gly Thr Val Ser Pro
 595 600 605
 Thr Ser Tyr Asn Val Ile Ser Asp Asn Met Gly Leu Asn Ala Asp Lys
 610 615 620
 Leu Gln Met Leu Ser Tyr Lys Met Thr His Met Tyr Tyr Asn Tyr Ser
 625 630 635 640
 Gly Thr Ile Arg Val Pro Ala Val Cys His Tyr Ala His Lys Leu Ala
 645 650 655
 Phe Leu Val Ala Glu Ser Ile Asn Arg Ala Pro Ser Ala Gly Leu Gln
 660 665 670
 Asn Gln Leu Tyr Phe Leu
 675

<210> 8
 <211> 69

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence

<221> VARIANT
 <222> 2, 3, 4, 6, 8, 9, 12, 13, 14, 15, 16, 17, 18, 19, 21,
 22, 23, 24, 26, 29, 31, 32, 33, 35, 36, 37, 39, 40,
 41, 44, 45, 46, 47, 49, 51, 55, 56, 59, 60, 63, 64,
 67, 68

<223> Xaa = Any Amino Acid

<221> VARIANT
 <222> 10, 25, 43

<223> Xaa = Any amino Acid if present

<400> 8

Pro	Xaa	Xaa	Xaa	Leu	Xaa	Glu	Xaa	Xaa	Xaa	Gln	Xaa	Xaa	Xaa	Xaa	Xaa
1							5				10				15
Xaa	Xaa	Xaa	Tyr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Pro	Xaa	His	Xaa	Xaa
			20							25				30	
Xaa	Phe	Xaa	Xaa	Xaa	Val	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Gly
	35						40			45					
Xaa	Gly	Xaa	Ser	Lys	Lys	Xaa	Xaa	Ala	Lys	Xaa	Xaa	Ala	Ala	Xaa	Xaa
	50						55			60					
Ala	Leu	Xaa	Xaa	Leu											
	65														

<210> 9
 <211> 766
 <212> PRT
 <213> Caenorhabditis elegans

<400> 9

Ser	Ala	Val	Glu	Arg	Gln	Phe	Ser	Val	Ser	Leu	Lys	Trp	Val	Gly	Gln
1								5				10			15
Val	Ser	Leu	Ser	Thr	Leu	Glu	Asp	Ala	Met	Glu	Gly	Arg	Val	Arg	Gln
				20					25			30			
Val	Pro	Phe	Glu	Ala	Val	Gln	Ala	Met	Asp	Val	Ile	Leu	Arg	His	Leu
		35						40			45				
Pro	Ser	Leu	Lys	Tyr	Thr	Pro	Val	Gly	Arg	Ser	Phe	Phe	Ser	Pro	Pro
	50						55			60					
Val	Pro	Asn	Ala	Ser	Gly	Val	Met	Ala	Gly	Ser	Cys	Pro	Pro	Gln	Ala
	65						70			75				80	
Ser	Gly	Ala	Val	Ala	Gly	Gly	Ala	His	Ser	Ala	Gly	Gln	Tyr	His	Ala
						85			90				95		
Glu	Ser	Lys	Leu	Gly	Gly	Arg	Glu	Val	Trp	Phe	Gly	Phe	His	Gln	
						100			105			110			
Ser	Val	Arg	Pro	Ser	Gln	Trp	Lys	Met	Met	Leu	Asn	Ile	Asp	Val	Ser
	115							120			125				
Ala	Thr	Ala	Phe	Tyr	Arg	Ser	Met	Pro	Val	Ile	Glu	Phe	Ile	Ala	Glu
	130						135			140					
Val	Leu	Glu	Leu	Pro	Val	Gln	Ala	Leu	Ala	Glu	Arg	Arg	Ala	Leu	Ser
	145						150			155				160	
Asp	Ala	Gln	Arg	Val	Lys	Phe	Thr	Lys	Glu	Ile	Arg	Gly	Leu	Lys	Ile
							165			170			175		
Glu	Ile	Thr	His	Cys	Gly	Gln	Met	Arg	Arg	Lys	Tyr	Arg	Val	Cys	Asn
							180			185			190		

Val Thr Arg Arg Pro Ala Gln Thr Gln Thr Phe Pro Leu Gln Leu Glu
 195 200 205
 Thr Gly Gln Thr Ile Glu Cys Thr Val Ala Lys Tyr Phe Tyr Asp Lys
 210 215 220
 Tyr Arg Ile Gln Leu Lys Tyr Pro His Leu Pro Cys Leu Gln Val Gly
 225 230 235 240
 Gln Glu Gln Lys His Thr Tyr Leu Pro Pro Glu Val Cys Asn Ile Val
 245 250 255
 Pro Gly Gln Arg Cys Ile Lys Lys Leu Thr Asp Val Gln Thr Ser Thr
 260 265 270
 Met Ile Lys Ala Thr Ala Arg Ser Ala Pro Glu Arg Glu Arg Glu Ile
 275 280 285
 Ser Asn Leu Val Arg Lys Ala Glu Phe Ser Ala Asp Pro Phe Ala His
 290 295 300
 Glu Phe Gly Ile Thr Ile Asn Pro Ala Met Thr Glu Val Lys Gly Arg
 305 310 315 320
 Val Leu Ser Ala Pro Lys Leu Leu Tyr Gly Gly Arg Thr Arg Ala Thr
 325 330 335
 Ala Leu Pro Asn Gln Gly Val Trp Asp Met Arg Gly Lys Gln Phe His
 340 345 350
 Thr Gly Ile Asp Val Arg Val Trp Ala Ile Ala Cys Phe Ala Gln Gln
 355 360 365
 Gln His Val Lys Glu Asn Asp Leu Arg Met Phe Thr Asn Gln Leu Gln
 370 375 380
 Arg Ile Ser Asn Asp Ala Gly Met Pro Ile Val Gly Asn Pro Cys Phe
 385 390 395 400
 Cys Lys Tyr Ala Val Gly Val Glu Gln Val Glu Pro Met Phe Lys Tyr
 405 410 415
 Leu Lys Gln Asn Tyr Ser Gly Ile Gln Leu Val Val Val Val Leu Pro
 420 425 430
 Gly Lys Thr Pro Val Tyr Ala Glu Val Lys Arg Val Gly Asp Thr Val
 435 440 445
 Leu Gly Ile Ala Thr Gln Cys Val Gln Ala Lys Asn Ala Ile Arg Thr
 450 455 460
 Thr Pro Gln Thr Leu Ser Asn Leu Cys Leu Lys Met Asn Val Lys Leu
 465 470 475 480
 Gly Gly Val Asn Ser Ile Leu Leu Pro Asn Val Arg Pro Arg Ile Phe
 485 490 495
 Asn Glu Pro Val Ile Phe Phe Gly Cys Asp Ile Thr His Pro Pro Ala
 500 505 510
 Gly Asp Ser Arg Lys Pro Ser Ile Ala Ala Val Val Gly Ser Met Asp
 515 520 525
 Ala His Pro Ser Arg Tyr Ala Ala Thr Val Arg Val Gln Gln His Arg
 530 535 540
 Gln Glu Ile Ile Ser Asp Leu Thr Tyr Met Val Arg Glu Leu Leu Val
 545 550 555 560
 Gln Phe Tyr Arg Asn Thr Arg Phe Lys Pro Ala Arg Ile Val Val Tyr
 565 570 575
 Arg Asp Gly Val Ser Glu Gly Gln Phe Phe Asn Val Leu Gln Tyr Glu
 580 585 590
 Leu Arg Ala Ile Arg Glu Ala Cys Met Met Leu Glu Arg Gly Tyr Gln
 595 600 605
 Pro Gly Ile Thr Phe Ile Ala Val Gln Lys Arg His His Thr Arg Leu
 610 615 620
 Phe Ala Val Asp Lys Lys Asp Gln Val Gly Lys Ala Tyr Asn Ile Pro
 625 630 635 640
 Pro Gly Thr Thr Val Asp Val Gly Ile Thr His Pro Thr Glu Phe Asp
 645 650 655
 Phe Tyr Leu Cys Ser His Ala Gly Ile Gln Gly Thr Ser Arg Pro Ser
 660 665 670
 His Tyr His Val Leu Trp Asp Asp Asn Asn Leu Thr Ala Asp Glu Leu

675	680	685
Gln Gln Leu Thr Tyr Gln Met Cys His Thr Tyr Val Arg Cys Thr Arg		
690	695	700
Ser Val Ser Ile Pro Ala Pro Ala Tyr Tyr Ala His Leu Val Ala Phe		
705	710	715
Arg Ala Arg Tyr His Leu Val Asp Arg Glu His Asp Ser Gly Glu Gly		
725	730	735
Ser Gln Pro Ser Gly Thr Ser Glu Asp Thr Thr Leu Ser Asn Met Ala		
740	745	750
Arg Ala Val Gln Val Ile Leu Ala Phe Asn Leu Val Ser Ile		
755	760	765
<210> 10		
<211> 737		
<212> PRT		
<213> Oryctolagus cuniculus		
<400> 10		
Gly Lys Asp Arg Ile Phe Lys Val Ser Ile Lys Trp Val Ser Cys Val		
1	5	10
Ser Leu Gln Ala Leu His Asp Ala Leu Ser Gly Arg Leu Pro Ser Val		
20	25	30
Pro Phe Glu Thr Ile Gln Ala Leu Asp Val Val Met Arg His Leu Pro		
35	40	45
Ser Met Arg Tyr Thr Pro Val Gly Arg Ser Phe Phe Thr Ala Ser Glu		
50	55	60
Gly Cys Ser Asn Pro Leu Gly Gly Arg Glu Val Trp Phe Gly Phe		
65	70	75
His Gln Ser Val Arg Pro Ser Leu Trp Lys Met Met Leu Asn Ile Asp		
85	90	95
Val Ser Ala Thr Ala Phe Tyr Lys Ala Gln Pro Val Ile Glu Phe Val		
100	105	110
Cys Glu Val Leu Asp Phe Lys Ser Ile Glu Glu Gln Gln Lys Pro Leu		
115	120	125
Thr Asp Ser Gln Arg Val Lys Phe Thr Lys Glu Ile Lys Gly Leu Lys		
130	135	140
Val Glu Ile Thr His Cys Gly Gln Met Lys Arg Lys Tyr Arg Val Cys		
145	150	155
Asn Val Thr Arg Arg Pro Ala Ser His Gln Thr Phe Pro Leu Gln Gln		
165	170	175
Glu Ser Gly Gln Thr Val Glu Cys Thr Val Ala Gln Tyr Phe Lys Asp		
180	185	190
Arg His Lys Leu Val Leu Arg Tyr Pro His Leu Pro Cys Leu Gln Val		
195	200	205
Gly Gln Glu Gln Lys His Thr Tyr Leu Pro Leu Glu Val Cys Asn Ile		
210	215	220
Val Ala Gly Gln Arg Cys Ile Lys Lys Leu Thr Asp Asn Gln Thr Ser		
225	230	235
Thr Met Ile Arg Ala Thr Ala Arg Ser Ala Pro Asp Arg Gln Glu Glu		
245	250	255
Ile Ser Lys Leu Met Arg Ser Ala Ser Phe Asn Thr Asp Pro Tyr Val		
260	265	270
Arg Glu Phe Gly Ile Met Val Lys Asp Glu Met Thr Asp Val Thr Gly		
275	280	285
Arg Val Leu Gln Pro Pro Ser Ile Leu Tyr Gly Gly Arg Asn Lys Ala		
290	295	300
Ile Ala Thr Pro Val Gln Gly Val Trp Asp Met Arg Asn Lys Gln Phe		
305	310	315
His Thr Gly Ile Glu Ile Lys Val Trp Ala Ile Ala Cys Phe Ala Pro		
325	330	335
Gln Arg Gln Cys Thr Glu Val His Leu Lys Ser Phe Thr Glu Gln Leu		

	340	345	350
Arg Lys Ile Ser Arg Asp Ala Gly Met Pro Ile Gln Gly Gln Pro Cys			
355	360	365	
Phe Cys Lys Tyr Ala Gln Gly Ala Asp Ser Val Gly Pro Met Phe Arg			
370	375	380	
His Leu Lys Asn Thr Tyr Ala Gly Leu Gln Leu Val Val Val Ile Leu			
385	390	395	400
Pro Gly Lys Thr Pro Val Tyr Ala Glu Val Lys Arg Val Gly Asp Thr			
405	410	415	
Val Leu Gly Met Ala Thr Gln Cys Val Gln Met Lys Asn Val Gln Arg			
420	425	430	
Thr Thr Pro Gln Thr Leu Ser Asn Leu Cys Leu Lys Ile Asn Val Lys			
435	440	445	
Leu Gly Gly Val Asn Asn Ile Leu Leu Pro Gln Gly Arg Pro Pro Val			
450	455	460	
Phe Gln Gln Pro Val Ile Phe Leu Gly Ala Asp Val Thr His Pro Pro			
465	470	475	480
Ala Gly Asp Gly Lys Lys Pro Ser Ile Ala Ala Val Val Gly Ser Met			
485	490	495	
Asp Ala His Pro Asn Arg Tyr Cys Ala Thr Val Arg Val Gln Gln His			
500	505	510	
Arg Gln Glu Ile Ile Gln Asp Leu Ala Ala Met Val Arg Glu Leu Leu			
515	520	525	
Ile Gln Phe Tyr Lys Ser Thr Arg Phe Lys Pro Thr Arg Ile Ile Phe			
530	535	540	
Tyr Arg Asp Gly Val Ser Glu Gly Gln Phe Gln Gln Val Leu His His			
545	550	555	560
Glu Leu Leu Ala Ile Arg Glu Ala Cys Ile Lys Leu Glu Lys Asp Tyr			
565	570	575	
Gln Pro Gly Ile Thr Phe Ile Val Val Gln Lys Arg His His Thr Arg			
580	585	590	
Leu Phe Cys Thr Asp Lys Asn Glu Arg Val Gly Lys Ser Gly Asn Ile			
595	600	605	
Pro Ala Gly Thr Thr Val Asp Thr Lys Ile Thr His Pro Thr Glu Phe			
610	615	620	
Asp Phe Tyr Leu Cys Ser His Ala Gly Ile Gln Gly Thr Ser Arg Pro			
625	630	635	640
Ser His Tyr His Val Leu Trp Asp Asp Asn Arg Phe Ser Ser Asp Glu			
645	650	655	
Leu Gln Ile Leu Thr Tyr Gln Leu Cys His Thr Tyr Val Arg Cys Thr			
660	665	670	
Arg Ser Val Ser Ile Pro Ala Pro Ala Tyr Tyr Ala His Leu Val Ala			
675	680	685	
Phe Arg Ala Arg Tyr His Leu Val Asp Lys Glu His Asp Ser Ala Glu			
690	695	700	
Gly Ser His Thr Ser Gly Gln Ser Asn Gly Arg Asp His Gln Ala Leu			
705	710	715	720
Ala Lys Ala Val Gln Val His Gln Asp Thr Leu Arg Thr Met Tyr Phe			
725	730	735	
Ala			

<210> 11
<211> 66
<212> PRT
<213> Xenopus laevis

<400> 11
Pro Val Gly Ser Leu Gln Glu Leu Ala Val Gln Lys Gly Trp Arg Leu
1 5 10 15
Pro Glu Tyr Thr Val Ala Gln Glu Ser Gly Pro Pro His Lys Arg Glu

	20	25	30												
Phe	Thr	Ile	Thr	Cys	Arg	Val	Glu	Thr	Phe	Val	Glu	Thr	Gly	Ser	Gly
	35				40							45			
Thr	Ser	Lys	Gln	Val	Ala	Lys	Arg	Val	Ala	Ala	Glu	Lys	Leu	Leu	Thr
	50				55							60			
Lys	Phe														
	65														
<210> 12															
<211> 66															
<212> PRT															
<213> Homo sapiens															
<400> 12															
Phe	Met	Glu	Glu	Leu	Asn	Thr	Tyr	Arg	Gln	Lys	Gln	Gly	Val	Val	Leu
	1			5					10				15		
Lys	Tyr	Gln	Glu	Leu	Pro	Asn	Ser	Gly	Pro	Pro	His	Asp	Arg	Arg	Phe
	20				25								30		
Thr	Phe	Gln	Val	Ile	Ile	Asp	Gly	Arg	Glu	Phe	Pro	Glu	Gly	Glu	Gly
	35				40							45			
Arg	Ser	Lys	Lys	Glu	Ala	Lys	Asn	Ala	Ala	Ala	Lys	Leu	Ala	Val	Glu
	50				55							60			
Ile	Leu														
	65														
<210> 13															
<211> 818															
<212> PRT															
<213> Caenorhabditis elegans															
<400> 13															
Val	Asn	Glu	Glu	Ile	Lys	Val	Gln	Phe	Ala	Lys	Asn	Phe	Val	Tyr	Asp
	1				5				10				15		
Asn	Asn	Ser	Ile	Leu	Arg	Val	Pro	Glu	Ser	Phe	His	Asp	Pro	Asn	Arg
	20				25				30						
Phe	Glu	Gln	Ser	Leu	Glu	Val	Ala	Pro	Arg	Ile	Glu	Ala	Trp	Phe	Gly
	35				40						45				
Ile	Tyr	Ile	Gly	Ile	Lys	Glu	Leu	Phe	Asp	Gly	Glu	Pro	Val	Leu	Asn
	50				55						60				
Phe	Ala	Ile	Val	Asp	Lys	Leu	Phe	Tyr	Asn	Ala	Pro	Lys	Met	Ser	Leu
	65				70				75				80		
Leu	Asp	Tyr	Leu	Leu	Ile	Val	Asp	Pro	Gln	Ser	Cys	Asn	Asp	Asp	
	85				90						95				
Val	Arg	Lys	Asp	Leu	Lys	Thr	Lys	Leu	Met	Ala	Gly	Lys	Met	Thr	Ile
	100				105				110						
Arg	Gln	Ala	Ala	Arg	Pro	Arg	Ile	Arg	Gln	Leu	Leu	Glu	Asn	Leu	Lys
	115				120					125					
Leu	Lys	Cys	Ala	Glu	Val	Trp	Asp	Asn	Glu	Met	Ser	Arg	Leu	Thr	Glu
	130				135					140					
Arg	His	Leu	Thr	Phe	Leu	Asp	Leu	Cys	Glu	Glu	Asn	Ser	Leu	Val	Tyr
	145				150				155				160		
Lys	Val	Thr	Gly	Lys	Ser	Asp	Arg	Gly	Arg	Asn	Ala	Lys	Lys	Tyr	Asp
	165				170				175						
Thr	Thr	Leu	Phe	Lys	Ile	Tyr	Glu	Glu	Asn	Lys	Lys	Phe	Ile	Glu	Phe
	180				185					190					
Pro	His	Leu	Pro	Leu	Val	Lys	Val	Lys	Ser	Gly	Ala	Lys	Glu	Tyr	Ala
	195				200					205					
Val	Pro	Met	Glu	His	Leu	Glu	Val	His	Glu	Lys	Pro	Gln	Arg	Tyr	Lys
	210				215					220					
Asn	Arg	Ile	Asp	Leu	Val	Met	Gln	Asp	Lys	Phe	Leu	Lys	Arg	Ala	Thr
	225				230				235				240		

Arg Lys Pro His Asp Tyr Lys Glu Asn Thr Leu Lys Met Leu Lys Glu
 245 250 255
 Leu Asp Phe Ser Ser Glu Glu Leu Asn Phe Val Glu Arg Phe Gly Leu
 260 265 270
 Cys Ser Lys Leu Gln Met Ile Glu Cys Pro Gly Lys Val Leu Lys Glu
 275 280 285
 Pro Met Leu Val Asn Ser Val Asn Glu Gln Ile Lys Met Thr Pro Val
 290 295 300
 Ile Arg Gly Phe Gln Glu Lys Gln Leu Asn Val Val Pro Glu Lys Glu
 305 310 315 320
 Leu Cys Cys Ala Val Phe Val Val Asn Glu Thr Ala Gly Asn Pro Cys
 325 330 335
 Leu Glu Glu Asn Asp Val Val Lys Phe Tyr Thr Glu Leu Ile Gly Gly
 340 345 350
 Cys Lys Phe Arg Gly Ile Arg Ile Gly Ala Asn Glu Asn Arg Gly Ala
 355 360 365
 Gln Ser Ile Met Tyr Asp Ala Thr Lys Asn Glu Tyr Ala Phe Tyr Lys
 370 375 380
 Asn Cys Thr Leu Asn Thr Gly Ile Gly Arg Phe Glu Ile Ala Ala Thr
 385 390 395 400
 Glu Ala Lys Asn Met Phe Glu Arg Leu Pro Asp Lys Glu Gln Lys Val
 405 410 415
 Leu Met Phe Ile Ile Ser Lys Arg Gln Leu Asn Ala Tyr Gly Phe
 420 425 430
 Val Lys His Tyr Cys Asp His Thr Ile Gly Val Ala Asn Gln His Ile
 435 440 445
 Thr Ser Glu Thr Val Thr Lys Ala Leu Ala Ser Leu Arg His Glu Lys
 450 455 460
 Gly Ser Lys Arg Ile Phe Tyr Gln Ile Ala Leu Lys Ile Asn Ala Lys
 465 470 475 480
 Leu Gly Gly Ile Asn Gln Glu Leu Asp Trp Ser Glu Ile Ala Glu Ile
 485 490 495
 Ser Pro Glu Glu Lys Glu Arg Arg Lys Thr Met Pro Leu Thr Met Tyr
 500 505 510
 Val Gly Ile Asp Val Thr His Pro Thr Ser Tyr Ser Gly Ile Asp Tyr
 515 520 525
 Ser Ile Ala Ala Val Val Ala Ser Ile Asn Pro Gly Gly Thr Ile Tyr
 530 535 540
 Arg Asn Met Ile Val Thr Gln Glu Glu Cys Arg Pro Gly Glu Arg Ala
 545 550 555 560
 Val Ala His Gly Arg Glu Arg Thr Asp Ile Leu Glu Ala Lys Phe Val
 565 570 575
 Lys Leu Leu Arg Glu Phe Ala Glu Asn Asn Asp Asn Arg Ala Pro Ala
 580 585 590
 His Ile Val Val Tyr Arg Asp Gly Val Ser Asp Ser Glu Met Leu Arg
 595 600 605
 Val Ser His Asp Glu Leu Arg Ser Leu Lys Ser Glu Val Lys Gln Phe
 610 615 620
 Met Ser Glu Arg Asp Gly Glu Asp Pro Glu Pro Lys Tyr Thr Phe Ile
 625 630 635 640
 Val Ile Gln Lys Arg His Asn Thr Arg Leu Leu Arg Arg Met Glu Lys
 645 650 655
 Asp Lys Pro Val Val Asn Lys Asp Leu Thr Pro Ala Glu Thr Asp Val
 660 665 670
 Ala Val Ala Ala Val Lys Gln Trp Glu Glu Asp Met Lys Glu Ser Lys
 675 680 685
 Glu Thr Gly Ile Val Asn Pro Ser Ser Gly Thr Thr Val Asp Lys Leu
 690 695 700
 Ile Val Ser Lys Tyr Lys Phe Asp Phe Phe Leu Ala Ser His His Gly
 705 710 715 720
 Val Leu Gly Thr Ser Arg Pro Gly His Tyr Thr Val Met Tyr Asp Asp

725 730 735
Lys Gly Met Ser Gln Asp Glu Val Tyr Lys Met Thr Tyr Gly Leu Ala
740 745 750
Phe Leu Ser Ala Arg Cys Arg Lys Pro Ile Ser Leu Pro Val Pro Val
755 760 765
His Tyr Ala His Leu Ser Cys Glu Lys Ala Lys Glu Leu Tyr Arg Thr
770 775 780
Tyr Lys Glu His Tyr Ile Gly Asp Tyr Ala Gln Pro Arg Thr Arg His
785 790 795 800
Glu Met Glu His Phe Leu Gln Thr Asn Val Lys Tyr Pro Gly Met Ser
805 810 815
Phe Ala

<210> 14
<211> 63
<212> PRT
<213> *Caenorhabditis elegans*

<400> 14
Trp Val Gly Lys Leu Gln Phe Lys Ser Gln Lys Ser Lys Leu Gln Ala
1 5 10 15
Asp Ile Tyr Glu Asp Ser Lys Asn Glu Arg Thr Glu Phe Thr Leu Val
20 25 30
Ile Cys Thr Met Cys Asn Gln Lys Thr Arg Gly Ile Thr Ser Lys Gln
35 40 45
Lys Asp Ala Lys Asn Leu Ala Ala Trp Leu Met Trp Lys Ala Leu
50 55 60